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(2) Applicants have amended the specification by replacing the paragraph that begins at line 30 of page 6 and ends at line 9 of page 7 in order to provide the full citation for a reference originally disclosed as "in press". The full citation can be found in the specification as filed at p. 39, lines 4 - 5; accordingly, no new matter has been added.

(3) Applicants have amended the specification by replacing the paragraph that begins at line 33 of page 23 and ends at line 8 of page 25 (i) to bring the serial number of applicants' GB priority application into conformity with the practice of the respective foreign patent office, adding the required prefatory two digit year designator to the serial number as originally set forth in the specification of the instant application as filed, and (ii) to replace the docket number, filing date, and title, for each of applicants' ten international priority applications with their respective application serial numbers. No new matter has been added.

(4) Applicants have amended the specification by replacing the paragraph that begins at line 28 of page 76 and ends at line 3 of page 77 in order to adjust the font, thus clarifying that the lower case "e" in the BLAST expect ("E") values signals base 10 exponentiation. The intent of the original font would readily have been understood by the skilled artisan familiar with BLAST, and is in accord with the parenthetical equivalences set forth in the specification as filed at page 11, lines 4 - 7; accordingly, no new matter has been added.

(5) Applicants have amended the specification by replacing the paragraph that begins at line 26 of page 80 and ends at line 10 of page 81 to adjust the font, thus

clarifying that the lower case "e" in the BLAST expect ("E") values signals base 10 exponentiation. The intent of the original font would readily have been understood by the skilled artisan familiar with BLAST, and is in accord with the parenthetical equivalences set forth in the specification as filed at page 11, lines 4 - 7; accordingly, no new matter has been added.

(6) Applicants have amended the specification by replacing the paragraph at lines 7 - 16 of page 82 to adjust the font, thus clarifying that the lower case "e" in the BLAST expect ("E") values signals base 10 exponentiation. The intent of the original font would readily have been understood by the skilled artisan familiar with BLAST, and is in accord with the parenthetical equivalences set forth in the specification as filed at page 11, lines 4 - 7; accordingly, no new matter has been added. The applicants have further amended the paragraph to replace reference to a blue line with reference to a solid line, a change occasioned by rendering of the color figure in black and white. The reference is unambiguous, inasmuch as (i) there are only two lines, the other of which is correctly identified, and (ii) the line is identified as solid in the specification as filed at page 11, line 5.

(7) Applicants have amended the specification by replacing the paragraph that begins at line 18 of page 96 and ends at line 22 of page 97 (i) to bring the serial number of applicants' GB priority application into conformity with the practice of the respective foreign patent office, adding the required prefatory two digit year designator to the serial number as originally set forth in the specification of the instant application as filed, and (ii) to replace the docket number, filing date, and title, for each of applicants' ten

international priority applications with their respective application serial numbers. No new matter has been added.

(8) Applicants have amended the specification by replacing the paragraph that begins at line 12 of page 98 and ends at line 13 of page 99 (i) to bring the serial number of applicants' GB priority application into conformity with the practice of the respective foreign patent office, adding the required prefatory two digit year designator to the serial number as originally set forth in the specification of the instant application as filed, and (ii) to replace the docket number, filing date, and title, for each of applicants' ten international priority applications with their respective application serial numbers. No new matter has been added.

Amendments to the Claims

Applicants herein add new claims 21 - 92 more particularly to point out and distinctly claim applicants' invention. Support for new claims 21 - 92 can be found throughout the specification, and particularly as set forth below. No new matter has been added.

Claims 21 - 53

**Claims 21 - 52** are drawn to a high throughput microarray-based method to confirm predicted exons, comprising detecting hybridization by transcript-derived nucleic acids to microarray probes that include genomic sequence predicted to contribute to no more than one exon, whereby detectable hybridization confirms the prediction of the exon included in each of the detectably hybridized probes. **Claim 53** is drawn to the converse, a method of identifying potential false positive exon predictions,

whereby absence of detectable hybridization in the method of claim 21 identifies as a potential false positive the exon predicted in each undetectably hybridized probe. Support for the methods can be found throughout the specification and particularly between page 30, line 14 and page 60, line 18; in Examples 2 and 5; and in claims 15 - 18 as originally filed. Additional support for elements of dependent **claims 22 - 52** can be found throughout the specification and particularly as follows.

Support for the frequencies recited in **claims 22 - 24** can be found particularly at page 44, lines 9 - 20.

Support for application of the methods of the present invention to human genomic sequence, as recited in **claim 25**, is found throughout the specification and particularly at p. 61, lines 24 - 32; Examples 1, 2 and 5 with associated FIGS. 5 - 11; and at p. 18, lines 25 - 31; p. 20, lines 17 - 22; p. 24, line 33 - p. 25, line 8; p. 26, lines 14 - 22; p. 31, lines 6 - 16; p. 33, lines 7 - 10; p. 35, lines 6 - 9; p. 39, lines 11 - 19; and p. 55, lines 10 - 17. The aforedescribed locations are exemplary, not exhaustive.

Support for output of predictions from GenScan, Diction, Genefinder, and Grail, as recited in **claim 26** and **claim 27** can be found particularly in Examples 1, 2, and 5; p. 25, lines 24 - 28; p. 27, lines 21 - 24; p. 65, lines 28 - 33; and p. 94, lines 4 - 6.

Collective inclusion of exons predicted from all chromosomes of a eukaryotic organism, particularly a human being, as recited in **claims 28 and 29**, is particularly exemplified in Examples 1, 2 and 5.

Inclusion of probes that include exons predicted from human chromosome 22, as recited in **claim 30**, can be

found in Table 2's inclusion of AC006548-9, AC006548 mapping to homo sapiens chromosome 22q11.

Support for representation of each predicted exon by a plurality of probes, as recited in **claim 31**, can be found particularly at p. 38, lines 12 - 16.

Support for including between 5,000 and 19,000 probes on the microarray, as recited in **claim 32**, can be found particularly at p. 38, lines 7 - 9.

Support for **claim 33** can be found particularly at p. 29, line 19 to p. 30, line 2.

Support for the probe sizes recited in **claims 34 - 35** can be found particularly at p. 54, lines 5 - 14; p. 31, lines 8 - 16.

Support for amplification of probes from genomic DNA, as set forth in **claim 36**, can be found throughout the specification and particularly at p. 30, line 27 - p. 35, line 25; and Examples 1, 2, 4 and 5.

Support for chemical synthesis of probes, as recited in **claim 37**, can be found particularly at p. 32, lines 9 - 12; and p. 40, lines 15 - 18;

Noncovalent attachment of probes to the microarray substrate, as recited in **claim 38**, is exemplified in Examples 2 and 5, and is further particularly described at p. 36, lines 11 - 15; p. 46, lines 22 - 27. Covalent attachment of probes to the microarray substrate, as recited in **claim 39**, is particularly recited at p. 36, lines 11 - 12.

Use of ink jet technology for creation of the microarray, as recited in **claim 40**, is described particularly at p. 36, lines 24 - 26.

Use of glass slides as the microarray substrate, as set forth in **claim 41**, is exemplified in Examples 2 and 5, and also particularly described at p. 31, line 16; and p. 35, lines 26 - 27.

The additional, antecedent, method step recited in **claim 42** -- "contacting said microarray with at least a first sample of transcript-derived nucleic acids, said nucleic acids being detectably labeled" - is particularly described in Example 2; and p. 48, line 13 - p. 50, line 14. Use of labeled, particularly fluorescently labeled, first strand cDNA, as recited in **claims 43 and 44**, is particularly exemplified in Examples 2 and 5.

Particular support for labeling the transcript-derived nucleic acids, particularly first strand cDNAs, with Cy3 or Cy5, as recited in **claims 45 and 48**, can be found particularly in Examples 2 and 5, and additionally at p. 10, line 31; p. 50, lines 2 - 3; and p. 69, lines 18 - 20.

Concurrent two-color microarray hybridization, as recited in **claim 46**, is exemplified in Examples 2 and 5, and is further particularly described at p. 10, lines 7 - 12; and p. 69, lines 9 - 13.

Normalization of signals, as recited in **claim 47**, can be found particularly at p. 10, lines 31 - 33; p. 69, lines 28 - 31; Example 2 (particularly at p. 79, lines 28 - 32 and p. 82, lines 2 - 6); Example 5 (particularly at p. 96, lines 10 - 17). Background correction of signals, as further recited in **claim 47**, can be found particularly between p. 95, line 12, and page 96, line 9.

Use of a pooled nucleic acid control, particularly a pool that includes transcript-derived nucleic acids from a plurality of human cell lines, as recited in **claims 49 - 50**, can be found particularly at p. 49, lines 2 - 9; p. 78, lines 4 - 15.

Use of transcript-derived nucleic acids derived from cell lines and normal tissues, and particularly derived from a source within the group of human tissues and cell lines consisting of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa cells, BT474 cells and HBL

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100 cells, as recited in **claims 51 and 52**, is described particularly in Examples 2 and 5.

#### Claims 54 - 55

**Claims 54 and 55** are drawn to methods of identifying genes expressed by cells of a eukaryote averaging at least one intron per gene (**claim 54**), in particular human cells (**claim 55**), by hybridization of cDNA samples to single exon microarrays of the present invention, whereby the presence of a signal indicates the expression in the cell(s) from which the cDNA derives of a gene that comprises the exon of the signaling probe. Support can be found throughout the specification, particularly as set forth above for claims 21 - 53.

#### Claims 56 - 58

**Claims 56 - 58** are drawn to a high throughput, microarray-based method of grouping exons into a common gene based upon coregulated expression of exons predicted from a contiguous region of genomic DNA. Support for **claim 56** can be found particularly at p. 70, line 32 - p. 71, line 7.

#### Claims 59 - 81

**Claims 59 - 81**, which correspond to original claims 1 - 14, are drawn to single exon microarrays. Support for such microarrays is found throughout the specification, particularly including Examples 2, 4, and 5.

Additional support for various elements of **claim 59** can be found as follows. Exemplary high stringency conditions for microarray hybridization are described, *inter alia*, at page 54, lines 25 - 31; and p. 79, lines 10 - 16.

Particular support for exon microarrays from eukaryotic genomes having at least one intron per gene can be found at p. 48, lines 3 - 9 and in claim 1 as filed.

Additional support for various elements of **claim 60** can be found as follows. Support for microarrays having at least 5000 addressable probes can be found particularly at p. 38, lines 1 - 5. Support for inclusion of control probes can be found, *inter alia*, at p. 36, line 27 - p. 37, line 2; p. 76, lines 21 - 24; p. 95, line 12 - p. 96, line 9.

Additional support for various elements of **claim 61** can be found as follows. Support for the frequency of probes that have genomic sequence predicted to contribute to no more than a single exon can be found, *inter alia*, particularly at page 44, lines 9 - 20 and claim 1 as filed. Support for the average number of introns per gene can be found particularly at p. 47, line 12 - p. 48, line 9. Support for a minimum probe length of 50 nt can be found particularly at p. 54, lines 5 - 14.

Additional support for the frequencies recited in **claims 62 - 64** can be found particularly at page 44, lines 9 - 20.

Support for collective inclusion of exons predicted from all chromosomes of a eukaryotic organism, particularly a human being, as recited in **claims 65 - 67**, is particularly exemplified in Examples 1, 2 and 5.

Support for output of predictions from GenScan, Diction, Genefinder, and Grail, as recited in **claims 68 - 69** can be found particularly in Examples 1, 2, and 5; p. 25, lines 24 - 28; p. 27, lines 21 - 24; p. 65, lines 28 - 33; and p. 94, lines 4 - 6.

Support for representation of each predicted exon by a plurality of probes, as recited in **claim 70**, can be found particularly at p. 38, lines 12 - 16.

Support for including between 5,000 and 19,000 probes on the microarray, as recited in **claim 71**, can be found particularly at p. 38, lines 7 - 9.

Support for **claim 72** can be found particularly at p. 29, line 19 to p. 30, line 2

Support for amplification of probes of the microarray from genomic DNA, recited in **claim 73**, can be particularly be found exemplified in Examples 2, 4, and 5; and at p. 30, line 27 - p. 35, line 25.

Chemical synthesis of the probes of the microarray, as recited in **claim 74**, is particularly described in the specification at p. 32, lines 9 - 12; and p. 40, lines 15 - 18.

Noncovalent attachment of probes to the microarray substrate, as set forth in **claim 75**, is exemplified in Examples 2 and 5, and is further particularly described at p. 36, lines 11 - 15; p. 46, lines 22 - 27. Covalent attachment of probes to the microarray substrate, as recited in **claim 76**, is particularly recited at p. 36, lines 11 - 12.

Use of ink jet technology for creation of the microarray, as recited in **claim 77**, is described particularly at p. 36, lines 24 - 26.

Use of glass slides as the microarray substrate, as recited in **claim 78**, is exemplified in Examples 2 and 5, and also particularly described at p. 31, line 16; and p. 35, lines 26 - 27.

**Claim 79**, which recites that each of the probes is disposed on the array with its reverse complement, is supported throughout the specification's description of use of double-stranded amplified nucleic acids as probes, which double-stranded nucleic acids necessarily include the reverse complement of each of the two strands of the duplex. Further support can be found at p. 55, line 27 to p. 56, line 3.

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Use of control probes, as set forth in **claim 80**, is exemplified in Examples 2, 4, and 5, and is further described, *inter alia*, at p. 36, lines 27 - 32.

Claim 81 finds particular support in claim 5 as originally filed, and specification p. 32, lines 4 - 8; p. 33, lines 3 - 6; page 55, lines 10 - 17; and p. 56, lines 4 - 10.

### Claims 82 - 91

**Claims 82 - 91** are drawn to software data structures for annotating nucleic acid sequence with confirmed bioinformatic predictions. Support can be found throughout the specification, and particularly in FIG. 1; in the specification from page 16, line 33 to page 17, line 15; p. 60, line 19 - p. 61, line 23 (notably on p. 61, lines 9 - 23); from page 14, line 12 to p. 23, line 32 (particularly at p. 15, lines 1 - 15); in the data structure output embodiments as shown in Tables 1, 2, and 3; and in the data structure output embodiments (visual displays) described from line 1 of page 62 to line 17 of p. 72 and shown in FIGS. 3 - 4 and 9 - 10.

**Claims 83 - 85** particularly recite that the confirmed biological function is contribution of the genomic sequence to a mature mRNA transcript (*i.e.*, expression). Support can be found throughout the specification and particularly between page 30, line 14 and page 60, line 18; in the data structure output embodiments shown in FIGS. 3 - 4 and 9 - 10; and in Examples 2 and 5.

Common inclusion of confirmed prediction data in a single record with the sequence identifier, as recited in **claim 86**, is particularly described at p. 61, lines 15 - 17. Relating confirmed prediction data to the sequence identifier

by linking to a distinct record, as recited in **claim 87**, is particularly described at p. 61, lines 18 - 20.

Inclusion of sequence data itself, as recited in **claim 88**, is particularly described at p. 61, lines 13 - 15.

Support for inclusion within the sequence entries of software means for relating the sequence identifier to a measure of similarity to prior-accessioned sequences, as recited in **claim 89**, can be found particularly at p. 68, lines 13 - 33; and in the output embodiments shown in FIGS. 4, 8 and 9.

Support for inclusion in the sequence entries of software means for relating the sequence identifier to data that encode a textual description of similar, prior-accessioned nucleic acid sequences, as recited in **claim 90**, is particularly shown in the output embodiments of Table 2.

Inclusion in the sequence entries of software means for relating sequence identifiers to chromosomal map locations, as recited in **claim 91**, is found particularly in the description of the visual display output embodiments, particularly at p. 63, lines 21 - 25.

### Claim 92

Claim 92 is drawn to the product of the process of claim 56, an isolated nucleic acid having exons that have been commonly grouped by the referenced method. Support can be found as for claim 56.

Respectfully submitted,

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Attachment:

- Appendix Pursuant to 37 C.F.R. § 1.121(b)(1)(iii)

GOVERNMENT USE EDITION

Appendix Pursuant to 37 C.F.R. § 1.121(b)(1)(iii)

(1) Herewith, a marked up copy of the paragraph replacing that which begins at line 19 on page 5 and ends at line 5 of page 6:

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult.

Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher *et al.*, *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu *et al.*, *Genet. Eng.* 16:241-53 (1994); Uberbacher *et al.*, *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev *et al.*, *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev *et al.*, *Ismb* 5:294-302 (1997); and GEN[E]SCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998).

(2) Herewith, a marked up copy of the paragraph replacing that which begins at line 30 of page 6 and ends at line 9 of page 7:

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., "The I.M.A.G.E. Consortium: an Integrated Molecular Analysis of Genomes and Their Expression, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., [Cancer Res. (in press)]

Toxicologist 54:68-69 (2000). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

(3) Herewith, a marked up copy of the paragraph replacing that which begins at line 33 of page 23 and ends at line 8 of page 25:

As discussed below, and further described in detail in commonly owned and copending U.S. provisional application nos. 60/207,456, filed May 26, 2000; 60/234,687, filed September 21, 2000; 60/236,359, filed September 27, 2000; in commonly owned and copending U.K. patent application no. 0024263.6, filed October 4, 2000; and in commonly owned and copending PCT applications [filed January 29, 2001 (attorney docket nos. PB 0004 WO 1, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart"; PB 0004 WO 2, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human

brain"; PB 0004 WO 3, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver"; PB 0004 WO 4, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver"; PB 0004 WO 5, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung"; PB 0004 WO 6, "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow"; PB 0004 WO 7, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta"; PB 0004 WO 8, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in BT 474 cells"; PB 0004 WO 9, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in HBL 100 cells"; PB 0004 WO 10, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in Hela cells")] PCT/US01/00666; PCT/US01/00667; PCT/US01/00664; PCT/US01/00669; PCT/US01/00665; PCT/US01/00668; PCT/US01/00663; PCT/US01/00662; PCT/US01/00661; and PCT/US01/00670, the disclosures of which are incorporated herein by reference in their entirety, we have used the methods and apparatus of the present invention to identify more than 15,000 exons in human genomic sequence whose expression we have confirmed in at least one human tissue or cell type. Fully two-thirds of the exons belong to genes that were not at the time of our discovery represented in existing public expression (EST, cDNA) databases, making the methods and

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apparatus of the present invention extremely powerful tools for novel gene discovery.

(4) Herewith, a marked up copy of the paragraph replacing that which begins at line 28 of page 76 and ends at line 3 of page 77:

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("[E]E") values less than [1 e<sup>-100</sup>] 1e-100 (1 x 10<sup>-100</sup>)) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST [E]E values from [1 e<sup>-5</sup>] 1e-5 (1 x 10<sup>-5</sup>) to [1 e<sup>-99</sup>] 1e-99 (1 x 10<sup>-99</sup>)). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

(5) Herewith a marked-up copy of the paragraph replacing that which begins at line 26 of page 80 and ends at line 10 of page 81:

FIG. 7A is a matrix presenting the expression of all verified sequences that showed signal intensity greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression (expression ratio) of a clone in that tissue is indicated at the respective node

by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: [E] E values < [1e<sup>-100</sup>] 1e-100 (1 x 10<sup>-100</sup>); gray: [E] E values from [1e<sup>-5</sup>] 1e-5 (1 x 10<sup>-5</sup>) to [1e<sup>-99</sup>] 1e-99 (1 x 10<sup>-99</sup>); black: [E] E values > 1e<sup>-5</sup> (1 x 10<sup>-5</sup>)).

(6) Herewith a marked-up copy of the paragraph replacing that at lines 7 - 16 of page 82:

FIG. 8 shows in dashed line the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect [("E")] ("E") value of greater than [1e<sup>-30</sup>] 1e-30 (1 x 10<sup>-30</sup>) (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows [in blue] **solid line** the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than [1e<sup>-30</sup>] 1e-30 (1 x 10<sup>-30</sup>) ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

(7) Herewith a marked-up copy of the paragraph replacing that which begins at line 18 of page 96 and ends at line 22 of page 97:

Using this threshold, we identified over 15,000 single exon probes that produce significant signal in one or more of ten tested tissues/cell types. The exact structures of these single exon probes are clearly presented in the SEQUENCE LISTINGS included in commonly owned and copending U.S. provisional application nos. 60/207,456, filed May 26, 2000; 60/234,687, filed September 21, 2000; 60/236,359, filed September 27, 2000; in commonly owned and copending U.K. patent application no. 0024263.6, filed October 4, 2000; and in commonly owned and copending PCT applications [filed January 29, 2001 (attorney docket nos. PB 0004 WO 1, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart"; PB 0004 WO 2, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain"; PB 0004 WO 3, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver"; PB 0004 WO 4, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver"; PB 0004 WO 5, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung"; PB 0004 WO 6, "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow"; PB 0004 WO 7, for "Human genome-derived single exon nucleic

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acid probes useful for analysis of gene expression in human placenta"; PB 0004 WO 8, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in BT 474 cells"; PB 0004 WO 9, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in HBL 100 cells"; PB 0004 WO 10, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in Hela cells"),] PCT/US01/00666; PCT/US01/00667; PCT/US01/00664; PCT/US01/00669; PCT/US01/00665; PCT/US01/00668; PCT/US01/00663; PCT/US01/00662; PCT/US01/00661; and PCT/US01/00670, the disclosures of which are incorporated herein by reference in their entireties.

(8) Herewith a marked-up copy of the paragraph replacing that which begins at line 12 of page 98 and ends at line 13 of page 99:

The exact structures of these single exon probes are clearly presented in the SEQUENCE LISTINGS included in commonly owned and copending U.S. provisional application nos. 60/207,456, filed May 26, 2000; 60/234,687, filed September 21, 2000; 60/236,359, filed September 27, 2000; in commonly owned and copending U.K. patent application no. 0024263.6, filed October 4, 2000; and in commonly owned and copending PCT applications [filed January 29, 2001 (attorney docket nos. PB 0004 WO 1, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human heart"; PB 0004 WO 2, for "Human genome-

derived single exon nucleic acid probes useful for analysis of gene expression in human brain"; PB 0004 WO 3, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver"; PB 0004 WO 4, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver"; PB 0004 WO 5, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung"; PB 0004 WO 6, "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow"; PB 0004 WO 7, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta"; PB 0004 WO 8, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in BT 474 cells"; PB 0004 WO 9, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in HBL 100 cells"; PB 0004 WO 10, for "Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in Hela cells"),] PCT/US01/00666; PCT/US01/00667; PCT/US01/00664; PCT/US01/00669; PCT/US01/00665; PCT/US01/00668; PCT/US01/00663; PCT/US01/00662; PCT/US01/00661; and PCT/US01/00670, the disclosures of which are incorporated herein by reference in their entireties.